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arched:
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 1, 2001, 09:29:30 ; Search time 60.99 Seconds Run on:

(without alignments) 119.849 Million cell updates/sec

1 MAFSGSQAPYLSPAVPFSGT......LPTINRLEVGGDIQLTHVQT 355 US-09-485-951-2 1917 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

197339 segs, 20590346 residues

197339 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_AA:\*

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ		•		
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	1633	85.2	311		TS-08-946-914-4	-
•	1	1	1	,	* *** 0** 00 00	TTAAU '* DOMENTO
~	783	40.8	149	7	US-08-788-584-3	Sequence 3, Appli
٣	661	34.5	145	7	US-08-788-584-1	1,
4	603.5	31.5	324	٣	US-08-946-914-11	11
z,	574	29.9	323	٦	US-08-469-667-16	16,
9	574	29.9	323	٣	US-08-946-914-2	2, A
7	574	29.9	323	ഗ	PCT-US95-07289-16	16,
80	3	27.9	145	7	US-08-788-584-5	5,
6	535	27.9	145	٣	US-08-946-914-12	12,
10	472.5	24.6	316	4	US-09-131-648-5	5
11	471.5	24.6	317	٣	US-08-946-914-6	9
12	454.5	23.7	316	7	US-08-728-521-3	ω,
13	454.5	23.7	316	7	US-08-647-960-2	7
14	454.5	23.7	316	٣	US-08-946-914-15	15,
15	454.5	23.7	316	٣	US-08-946-914-17	17,
16	353.5	18.4	264	7	US-08-728-521-1	1,
17	328.5	17.1	264	-	US-08-562-311-4	4
18	321.5	16.8	336	4	US-09-131-648-1	ī
19	321	16.7	262	٣	US-08-946-914-14	14
20	318.5	16.6	250	m	US-08-946-914-10	10
21	317.5	16.6	250	Н	US-08-562-311-2	2,
22	255	13.3	200	m	US-08-946-914-8	8,
23	254.5	13.3	177	7	US-08-647-960-6	9
24	250	13.0	147	7	US-08-647-960-7	7,
25	230.5	12.0	136	m	US-08-946-914-13	Sequence 13, Appl
56	226.5	11.8	135	7	US-08-647-960-5	2,
27	198.5	10.4	132	7	US-08-647-960-11	Ξ

Sequence 9, Appli Sequence 8, Appli	Sequence 18, Appl	Sequence 16, Appl Sequence 20, Appl	Sequence 2, Appl1 Patent No. 5242807		Sequence 3, Appl1	Seguence 16, Appl	Sequence 2, Appli	Patent No. 5470718	Sequence 17, Appl	Sequence 17, Appl	Sequence 17, Appl	Sequence 9, Appli
US-08-647-960-9 US-08-647-960-8	US-08-04/-900-10 US-08-050-259B-18	US-08-946-914-16 US-08-050-259B-20	US-U9-489-292-2 5242807-2	US-08-946-914-9	US-08-647-960-3	US-08-050-259B-16	US-08-540-202-2	5470718-4	US-08-220-151-17	US-08-413-118-17 ·	US-08-473-446-17	US-09-253-682-9
200	4 m c	n m ·	4 0	ი 4	0	m	Н	9	Н	Н	m	m
131	135	135	135	132	135	135	38	366	511	511	511	328
999		9 8 6	7 4.0	6.7	. w	5.7	5.6	5.5	5.0	5.0	5.0	4.9
189	167	154	142.5	129	112	108.5	107	105.5	96.5	96.5	96.5	94.5
7 7 7 8 8 7 8 8	31	3 8 6	3.5 3.5	36	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C. STREET: 1100 New York Ave., Suite 600 STREET: STATE: D.C. STATE: D.C.
                                                                                                                                                                                                                                                                                 COUNTY USA

COMPUTER READABLE FORM:

REDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36,688
ER: 1488.0560001/EKS/SGW
                                                                         GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFTCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                      Sequence 4, Application US/08946914
Patent No. 6027916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 202-371-2600
202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 311 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Steffe, Eric K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-946-914-4
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
RESULT 1
US-08-946-914-4
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Gaps Indels 44; Query Match 85.2%; Score 1633; DB 3; Best Local Similarity 87.6%; Pred. No. 3.2e-164; Matches 311; Conservative 0; Mismatches 0;

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1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

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Gaps

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MFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAF 266
                                                       Mismatches
   ;
0
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.5%;
Best Local Similarity 90.5%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                       RESULT 3
US-08-788-584-1
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                                      207
                                                                      Q
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                                                                       61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVWVNGILFV 120
                                                   61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
                                                                                                                       121 OYFHRVPFHRVDTISVNGSVQLSYISFONPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQK 180
                                                                                                                                                                                             181 PPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTLGGLYPSKS 240
                                                                                                                                                                                                                241 ILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPF 300
301 VRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355
                                                                                                                                                                                                                                                                                                                                                          Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 783; DB 2;
Pred. No. 5.1e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
OPERATING SYSTEM:
OSFTWARE: FastERD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,584
FILING DATE: Filed Herewith
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GOIL, SULYA K.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN GALECTINS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Incyte Pharmaceuticals, Inc
                                                                                                                                             REFERENCE/DOCKET NUMBER: PF-0192 US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08788584 Patent No. 5837493 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 149 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 FO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
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61 HLNPRFDENAVVRNTQIDNFWGSEERSLPRKMPFVRGGSFSVWILCEAHCLKVAVDGQHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 HLNPRFDENAVVRNTOIDNSWGSEERSLPRKMPFVRGOSFSVWILCEAHCLKVAVDGOHL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 PHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 RNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 3.6e-62;
3; Mismatches 10;
                                                                                                                                                                                                                                                  Sequence 1, Application US/08788584
Patent No. 5837493
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Petithory, Joanne R.
TITLE OF INVENTION: NOVEL HUMAN GALECTINS
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Incyte Pharmaceuticals, Inc.
                                                                                                                 121 FEYYHRLRNLPTINRLEVGGDIQLTHVQT 149
                                                                                       327 FEYYHRLRNLPTINRLEVGGDIQLTHVQT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/788,584
FILING DATE: Filed Herewith
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TVLPSAQRFHIN--LCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRG 303
215 YVLPTAKNLIINFKVGSTGDIAFHMNPRIGD-CVVRNSYMNGSWGSEERKIPYN-PFGAG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 DGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHRVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 FHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 YVPPTGKSFAINFKVGSSGDIALHINPRMGNGTVVRNSLLNGSWGSEEKKITHN-PFGPG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 PYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFS-GNDIAFHFNPRFF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPAPITQTVIHTVQSAPGQMFSTPAI - - PPMMYPHPAYPMPFITTILGGLYPSKSILLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 YPGP----GHCHQ----QLNSLPTMEGPPTFNP----PVPYFGRLQGGLTARRIIIKG
                                                                                      273 QFFDLSIRCGTDRFKVFANGQHLFDFSHRFQAFQRVDMLEIKGDITLSYVQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 323;
                                                              304 QSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQ
                                                                                                                                                                                                        Sequence 16, Application US/08469667
Patent No. 5733748
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   Carella, Byrne, Bain, Gilfillan, Cecchi,
Stewart & Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,667
FILING DATE: US-UN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.9%; Score 574; DB 1; L 38.2%; Pred. No. 1.9e-52; ive 52; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ferraro, Gregory D. REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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Matches 134; Conservative
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ZIP: 07068-1739
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                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                        US-08-469-667-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YP-----SAGYNPPOMNSLPVMAGPPIFNP----PVPYVGTLQGGLTARRTIIIKG 214
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                                                                                                                                                                                                                                                                                                                                                             Goldstein, & Fox P.L.L.C.
Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1488.0560001/EKS/SGW
                                                                                                                                                           Sequence 11, Application US/08946914
Patent No. 6027916
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
NUMBER OF SEQUENCES: 60
CORRESPONENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 603.5; DB 3 Pred. No. 1.4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, APPLICATION DATA: MS/08/946,914 FILING DATE: Herewith CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-0CT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                             1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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                                            129 INRLEVGGDIQLTHVQT 145
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                    339 INRLEVGGDIQLTHVQT
                                                                                                                                                                                                                                                                                                                                                                                                       Washington
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Best Local Similarity
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                                                                                                                        RESULT 4
US-08-946-914-11
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                     272 QFFDLSIRGGLDRFKVYANGQHLFDFAHRLSAFQRVDTLEIGGDVTLSYVQ 322
304 QSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQ 354
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Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1488.0560001/EKS/SGW
                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-0CT-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                Sequence 2, Application US/08946914 Patent No. 6027916 GENERAL INFORMATION:
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1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,689
REGISTRATION NUMBER: 146
REFERENCE/DOCKET NUMBER: 146
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
                                                                                                                                                                                                              APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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Best Local Similarity 38.2
Matches 134; Conservative
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70 GWDKVVFNTLQGGKWGSEERKRSMPFKKGAAFELVFIVLAEHYKVVVNGNPFYEYGHRLP 129
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213 YVPPTGKSFAINFKVGSSGDIALHINPRMGNGTVVRNSLLNGSWGSEEKKITHN-PFGPG 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 NPAPITQTVIHTVQSAPGQMFSTPAI - - PPMMYPHPAYPMPFITTILGGLYPSKSILLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                       304 QSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQ 354
                                               304 QSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQ 354
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38.2%; Pred. No. 1.9e-52;
ive 52; Mismatches 121; Indels
                                                                                                                                                                                                          Sequence 16, Application PC/TUS9507289
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERNCE/DOCKET NUMBER: 325800-265
TELECOMMUNICATION:
TELEPHONE: 201-994-1170N:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95/07289
FILING DATE: 06-JUN-1995
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 134; Conservative
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roseland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                         PCT-US95-07289-16
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208 FSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFH 267
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                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-0CT-1996
ATTONINY/AGENT INFORMATION:
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APPLICANT: Patterson, Chandra
APTLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1488.0560001/EKS/SGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%; Score 535; DB 3; illarity 70.3%; Pred. No. 7.2e-49; Conservative 9; Mismatches 29
                                                                                                                       8, 9, 10 and 10SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 EYYHRLRNLPTINRLEVGGDIQLTHVQT 355
                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: PatentIn PATENT
Sequence 12, Application US/08946914 Patent No. 6027916 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09131648
Patent No. 6168920
GENERAL INFORMATION
APPLICANT: Hillman, Jennifer L. APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
                                                        APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin
NUMBER OF SEQUENCES: 60
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                                                                                                                                                                                                                                                                          ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSE: Sterne, Ke
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Best Local Similarity
Matches 104; Conservi
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  Score 535; DB 2; Length 145;
Pred. No. 7.2e-49;
9; Mismatches 29; Indels
                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Petithory, Joanne R.
TITLE OF INVENTION: NVEL HUMAN GALECTINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE S.
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: Filed Herewith
CLASSIFICATION: 436
PRICR APPLICATION: A36
RENOR APPLICATION: A36
RENOR APPLICATION: A36
APPLICATION: NUMBER:
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NAME: Billings, Lucy J.
REGISTATION UNDBER: 36,749
REFERENCE/POCKET 186,749
RELECOMMUNICATION INFORMATION:
TELEFONE: 415-85-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEO ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                US-08-788-584-5; Sequence 5, Application US/08788584; Patent No. 5837493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 145 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                          Palo Alto
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LIBRARY: GenBa
CLONE: 727176
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US-08-946-914-12
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                                                                                                                                                                                                                                                                                               Indels 51; Gaps
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                                                                                                                                                                                                                                                            Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 SVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C. STREET: 1100 New York Ave., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        Query Match 24.6%; Score 472.5; DB 4; Best Local Similarity 33.0%; Pred. No. 9.2e-42; Matches 115; Conservative 55; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS:
CURRENT APPLICATION NUMBER: US/09/131,648 CURRENT FILING DATE: 1998-08-10 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,093
FILING DATE: 09-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 6, Application US/08946914
; Patent No. 6027916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                            ; OTHER INFORMATION: 91932712
US-09-131-648-5
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MEDIUM TYPE: Floppy
                                                                          SEQ ID NO 5
LENGTH: 316
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                           FEATURE: -
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69 GGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHRVPF 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 PSAQRFHINLCSG--NHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSF 306
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                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                               Length 317;
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res 128;
                                                                                                                                                                                                                                                                                                               DB 3;
                  REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                             ; Score 471.5; I; Pred. No. 1.2e-55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bandman, olga
APPLICANT: Bandman, olga
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: HUMAN GALECTIN HOMOLOG
CORRESPONDENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Incyte Pharmaceuticals, Inc.
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/728,521
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08728521
Patent No. 5869289
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
36,688
                                                                                                                                                                                                                                                                                                             Query Match 24.6%;
Best Local Similarity 33.0%;
Matches 115; Conservative 5
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COMPUTER: IBM Compatible
                                                                                                                                                 LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                              TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-946-914-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFS---GND 57
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APPLICANT: ZICK, Yehiel
APPLICANT: ZICK, Yehiel
TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                               23.7%; Score 454.5; DB 2; Length 31.7%; Pred. No. 7.3e-40; Live 62; Mismatches 133; Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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PF-0137 US
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APPLICATION NUMBER: US/08/647,960
FILING DATE: 30-MAY-1996
CLASSIFICATION: 536
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APPLICATION NUMBER: IL 107880
FILING DATE: 05-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08647960 Patent No. 5908761
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                  TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                        Matches 114; Conservative
                                                                                                                                                        single
                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
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CLONE: 717032
                                                                                                                                                      STRANDEDNESS:
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Suite 600
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                                                                                                                                                                                                                                                                                                23.7%; Score 454.5; DB 2;
31.7%; Pred. No. 7.3e-40;
Live 62; Mismatches 133;
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APPLICATION NUMBER: US 60/028,093
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6027916
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APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Galectin 8,
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                 NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ZICK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3527
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                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 LENGTH: 316 amino acids TYPE: amino acid
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-647-960-2
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Best Local Similarity
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US-08-946-914-15
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APPLICATION NUMBER

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31.7%; Pred. No. 7.3e-40;
ive 62; Mismatches 133;
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PPLICATION NUMBER: US/08/946,914
FILING DATE: Herewith
                                                                                                                                                         1488.0560001/EKS/SGW
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SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Ruben, Steven M.
ATILLE OF INVENTION: Galectin 8,
NUMBER OF SEQUENCES: 60
                                                                    NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REPRERNCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                              TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not relevant
FILING DATE: 09-OCT-1996 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 31.7%
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-946-914-15
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: no
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20005-3934
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61 VAFHFNPRFKRSNCIVCNTLTNEKWGWEEITHDMPFRKEKSFEIVIMVLKNKFHVAVNGK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 LEVQYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGR 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 SKSILLSGTVLPSAQRFHINLCSG--NHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFS---GND 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%; Score 454.5; DB 3;
31.7%; Pred. No. 7.3e-40;
live 62; Mismatches 133;
                                                                                                  1488.0560001/EKS/SGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 1, 2001, 09:29:31
Job time: 2307 sec
                                                                            36,688
                                                                                             REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                           TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID 0: 17:
SEQUENCE CHARACTERISTICS:
FILING DATE: 09-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,6
                                                                                                                                                                                                                                         316 amino acids
                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 31.79
Matches 114; Conservative
                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                         US-08-946-914-17
                                                                                                                                                                                                                                         LENGTH:
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.; 8

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

August 1, 2001, 09:42:18; Search time 36.57 Seconds (without alignments) 332.532 Million cell updates/sec Run on:

US-09-485-951-2 1917

1 MAFSGSQAPYLSPAVPFSGT.....LPTINRLEVGGDIQLTHVQT 355 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

93435 seqs, 34255486 residues arched:

Total number of hits satisfying chosen parameters:

93435

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	000182 homo sapien		008573 mus musculu	P38552 rattus norv	. P56470 homo sapien	Q29058 sus scrofa		O54891 mus musculu	Q9jl15 mus musculu	000214 homo sapien	Q62665 rattus norv			Q09581 caenorhabdi	_		P47845 oryctolagus	P16110 mus musculu	P08699 rattus norv	P17931 homo sapien	P47929 homo sapien	mus m	rattus	gallus	gallus	5 caenor	'n	_	P48538 cricetulus	P11762 rattus norv	Q09610 caenorhabdi	1116	P08520 electrophor
SUMMARIES	ID	LEG9_HUMAN	LEG9_RAT	LEG9_MOUSE	LEG4_RAT	LEG4_HUMAN	LEG4_PIG	LEG5_RAT	LEG6_MOUSE	LEG8_MOUSE	LEG8_HUMAN	LEG8_RAT	LEG1_HAECO	LE32_CAEEL	LE33_CAEEL		LEG3_CANFA	LEG3_RABIT	LEG3_MOUSE	LEG3_RAT	LEG3_HUMAN	LEG7_HUMAN	LEG7_MOUSE	LEG7_RAT	LEG6_CHICK	LEG4_CHICK	- 1	LEG1_MOUSE	LEG1_SHEEP	LEG1_CRIGR	LEG1_RAT	LEC8_CAEEL	LEG1_BOVIN	LEG_ELEEL
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	Length	355	354	353	324	323	323	144	301	316	316	316	283	279	285	244	295	241	263	261	249	135	135	135	134	134	182	134	134	134	134		134	129
œ	Ouery Match	10	71.7			29.9	28.3	27.9	27.0		24.2	٠.	22.3	•	5	۲.	17.2		16.8	16.7		12.0		٠					8.7					8.1
	Score	1917	1374.5	1324	603.5	574	541	535	518	467.5	463.5	454.5	427	414.5	374	339	330.5	324.5	322.5	321	318.5	230.5	223.5	216.5	189.5	184.5	182	167	166	164	164	164		155
	Result No.		7	Э	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

	Q05315 homo sapien Q92144 rattus norv								
LEG1_HUMAN	LPPL_HUMAN LEG2_RAT	LEGX_MOUSE	LEG2_HUMAN	LEG1_BUFAR	LEG2_PIG	YPX5_CAEEL	VGLD_PRVRI	LEG1_CONMY	YRN3_CAEEL
		7	П	٦	7	_	7	П	7
134	141	105	132	134	123	1216	402	135	536
8.0	7.5	7.0	6.7	6.5	6.4	6.1	0.9	5.9	5.8
154 144.5	144.5 141.5	135	129	125.5	123.5	117	115	113	111
34 35	36	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT LEGG_HUMAN LEGG_HUMAN LEGGG_HUMAN DT 101-00 DT 101-00 DT 101-00 DT 101-00 DS Bunkar OOS Bunk
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                                                                                                                                                                                                                                                                                                                               QYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQK 180
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                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF
                                                                                                                                                                                                                                                          181 PPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKS
                                                                                                                                                                                                                                                                                                                                                                                241.ILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPF
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0
                                                                                                    SIMILARITY).
                                                                                            SIMILARITY)
                                                                                                                                                                                                         Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 VRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT
                                                                                                                                                                                                                              Indels
                                                                                                             MISSING (IN SHORT ISOFORM)
                                                                                                                                                                         4748C22FCAFA536A CRC64;
                                                                               GALAPTIN 2.,
BETA-GALACTOSIDE (BY
BETA-GALACTOSIDE (BY
                                                                                                                      G -> S (IN REF. 3).
K -> R (IN REF. 1).
S -> F (IN REF. 1).
P -> L (IN REF. 1).
E -> G (IN REF. 1).
                                                                                                                                                                                                         Score 1917; DB 1;
Pred. No. 1.3e-146;
                                         GALAPIIN; 2.
Repeat; Alternative splicing.
                                                                                                                                                                                                                            0; Mismatches
                                                            GALAPTIN 1.
                                                                        LINKER
                InterPro; IPR001079; --
Pfam; PF00337; Gal-bind_lectin; 2.
PROSITE; PS00309; GALAPTIN; 2.
                                                                                                                                                                                                        100.0%;
                                                                                                                                                                           MM:
                                                                                                                                                                           39518
                                                                                                                                                                                                                             Conservative
                                                                       206
355
88
293
180
HSSP; P17931; 1A3K.
                                                                                                                                                                         355 AA;
                                                                                                                                                                                                                  Jest_Local Similarity
Matches 355; Conserv
                                                  Galaptin; Lectin;
                                                                                                             149
                                                                                                            VARSPLIC
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                         Query Match
                                                                                        BINDING
                                                                                                                                                                          SEQUENCE
                                                                    DOMAIN
                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                121
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                       Wada J., Kanwar Y.S.;
Identification and characterization of galectin-9, a novel beta-
galactoside-binding mammalian lectin.";
J. Biol. Chem. 272:6078-6086(1997).
P97840; 008588; 035866; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 35, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotation update) GALECTIN-9 (36 KDA BETA-GALACTOSIDE BINDING LECTIN) (URATE
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
STRAIN-SPRAGUE-DAWLEY, TISSUE-Kidney, and Small intestine;
MEDLINE-97190351; PubMed-9038233;
                                                                                             354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A. (SHORT FORM)
                                                                                                                                                                                        TRANSPORTER/CHANNEL) (UAT).
                                                                                             STANDARD;
                                                                                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                            LEG9_RAT
                                                                                                                                                                                                          LGALS9
```

1;

Gaps

68; Indels

DB 1; Length 354;

71.7%; Score 1374.5; DB 1 71.8%; Pred. No. 3.7e-103; 31; Mismatches

Matches 255; Conservative

Similarity

Query Match

Sest Local

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61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120 

1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60

ILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPF 300 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                      LIBIOL CHEM. 272:617-625(1997).

1. BIOL. CHEM. 272:617-625(1997).

1. FUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-
FPITHELIAL INTERACTIONS RELEVANT TO THE BIOLOGY OF THE THYMUS (BY
SIMILARITY). MAY PROVIDE THE MOLECULAR BASIS FOR URATE FLUX ACROSS
CELL MEMBRANES, ALLOWING URATE THAT IS FORMED DURING PURINE
METABOLISM TO EFFUX FROM CELLS AND SERVING AS AN ELECTROGENIC
TRANSPORTER THAT PLAYS AN IMPORTANT ROLE IN RENAL AND
GASTROINTESTINAL URATE EXCRETION. HIGHLY SELECTIVE TO THE ANION
                                                                                                                                                                                                                                                                                                       CLASSICAL SECRETORY PATHWAY (BY SIMILARITY).
-!- ATTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS, A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: THE LONG FORM IS EXPRESSED EXCLOSIVELY IN THE
                                                                                                                                                                                                                                                                                                                                                                                   SMALL INTESTINE.
-!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: CYTOPLASMIC. MAY ALSO BE SECRETED BY A NON-
                                   Leal-Pinto E., Tao W., Rappaport J., Richardson M., Knorr B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE.
6574F960B2EAF37C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Alternative splicing; Ion transport
                                                                          functional reconstitution of a urate
                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALAPTIN 1.
LINKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALAPTIN 2
STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney; MEDLINE-97150769; PubMed-8995305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00337; Gal-bind_lectin; 2. PS00309; GALAPTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205
354
GA
87
BE
292
BE
179
MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U59462; AAB51192.1; -. EMBL; U72741; AAB68592.1; -. EMBL; U67958; AAB48591.1; -.
                                                                        "Molecular cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001079;
                                                                                              transporter/channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P17931;
                                                         Abramson R.G.
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galaptin;
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Wed.Aug

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wada J., Kanwar Y.S.; "Identification and characterization of galectin-9, a novel beta-
LINKER.
GALAPTIN 2.
BETA CALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CD-1; TISSUE-Small intestine, and Kidney;
MEDLINE-97190351; PubMed-9038233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galaptin; Lectin; Repeat; Alternative splicing.
DOMAIN 1 147 GALAPTIN 1.
                                                                                                                                                                               LEG9_MOUSE STANDARD; PRT; 353 AA. 008572; 008572; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       galactoside-binding mammalian lectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 272:6078-6086(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:109496; Lgals9.
ItatPro: 1PR001079; -.
Pfam: PP00337; Gal-bind_lectin; 2.
PROSITE; PS00309; GALAPTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97298141; PubMed-9153289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U55061; AAB51190.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U55060; AAB51189.1; -.
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87
291
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                      GALECTIN-9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
BINDING
BINDING
                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93194902; PubMed=8449956; Oda Y., Herrmann J., Gitt M., Turck C.W., Burlingame A.L.,
Barondes S.H., Leffler H.;
"Soluble lactose-binding lectin from rat intestine with two different carbohydrate-binding domains in the same peptide.chain.";
J. Blod. Chem. 268:5929-5939(1993).
-i- FUNCTION: GALECTIN THAT BINDS LACTOSE AND A RELATED RANGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FULL-LENGTH FORM IN SMALL
AND LARGE INTESTINE AND STOMACH BUT WAS NOT DETECTED IN OTHER
TISSUES INCLUDING LUNG, LIVER, KIDNEY, AND SPLEEN
TISSUES INCLUDING LUNG, LIVER, KIDNEY, AND SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                      121 QYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQK 180
                                                                                                                                                                                                                                                                                                                                                                     181 PPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTLGGLYPSKS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ILLSGTVLPSAQRFHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPF 300
                                                                                                                                                                                                                     61 HFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFV 120
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                1 MAFSGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGNDIAF 60
                                                                                                                                                                 01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 VRGQSFSVWILCEAHCLKVAVDGOHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 SRGQSFSVWIIÇEGHCFKVAVNGQHMCEYYHRLKNLQDINTLEVAGDIQLTHVQT 353
                                                                                                           5
                                                                     Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                           69; Indels
 .78 MISSING (IN SHORT ISOFORM).
40036 MW; B54036F6E280C531 CRC64;
                                                                     69.1%; Score 1324; DB 1;
69.3%; Pred. No. 4.2e-99;
ive 38; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                           246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
148
353 AA;
                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUGARS
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P38552;
 VARSPLIC
                 SEQUENCE
                                                                       Query Match
Best Local (
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                                                                                                           Matches
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                          DGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHRVP 127
                                                                                                                                                                                                                                                                     128 FHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPA 187
                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                 245
                                                                                                                                                                                                                                                                                                                                                                      214
                                                                                                                                                                                                                                                                                                                                                                                             303
                                                                                                                                                                                                                                                                                                                                                                                                                  272
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                            9 PYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTG-FSGNDIAFHFNPRFF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Colorectal carcinoma; BEDLINE-97454307; PubMed-9310382; Rechreche H., Mallo G.V., Montalto G., Dagorn J.C., Iovanna J.L.; "Cloning and expression of the mRNA of human galectin-4, an S-type lectin down-regulated in colorectal cancer."; Bur. J. Blochem. 248:225-230(1997).

Fur. J. Blochem. 248:225-230(1997).

SUGARS. MAY BE INVOLVED IN THE ASSEMBLY OF ADHERENS JUNCTIONS.
                                                                                                                                                                                                                                                                                                                          130 LQMVTHLQVDGDLELQSINF----LGGQPAASQYPGTMTI-------PA
                                                                                                                                                                                                                                                                                                                                                NPAPITQTVIHTVQSAPGQMFSTPAI - - PPMMYPHPAYPMPFITTILGGLYPSKSILLSG
                                                                                                                                                                                                                                                                                                                                                                      168 YP-----SAGYNPPOMNSLPVMAGPPIFNP----PVPYVGTLQGGLTARRTIIIKG
                                                                                                                                                                                                                                                                                                                                                                                          TVLPSAQRFHINLCSGN--HIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRG
                                                                                                                                                                                                                                                                                                                                                                                                        215 VVLPTAKNLIINFKVGSTGDIAFHMNPRIGD-CVVRNSYMNGSWGSEERKIPPN-PFGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                          43;
                                                                                                                        BETA-GALACTOSIDE (BY SIMILARITY). 478024D7322AFE7B CRC64;
                                                                                                                                                                   Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 QFFDLSIRCGTDRFKVFANGQHLFDFSHRFQAFQRVDMLEIKGDITLSYVQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                     304 QSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQ 354
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                        Matches 139; Conservative 54; Mismatches 115;
                                                                                                                                                                   DB 1;
                                                                                                                                                                   31.5%; Score 603.5; DB 1 39.6%; Pred. No. 2.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AA
                                                                                        GALAPTIN 1.
                                                                                                              GALAPTIN 2.
                                                                                                   LINKER
                                         InterPro; IPR001079; -.
Pfam; PF00337; Gal-bind_lectin;
PROSTE; PS00309; GALAPIN; 2.
Galaptin; Lectin; Repeat.
                                                                                                                                  36347 MW;
           EMBL; M73553; AAA41505.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Gastric carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                           324
263
                    PIR; A46631; A46631.
HSSP; P17931: 1A3K
                                                                                                           178
257
324 AA;
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEG4_HUMAN
                                                                                                           DOMAIN
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (L36LBP).
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                                                                                                                                                                   Query Match
                                                                                                                                                                                Local
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                                                                                                   DOMAIN
                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
LEG4_HUMAN
                                                                                                                                                                                                                                                         89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
SUBUNIT: MONOMER (BY SIMILARITY).
DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GWDKVVFNTLQGGKWGSEERKRSMPFKKGAAFELVFIVLAEHYKVVVNGNPFYEYGHRLP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 LQMYTHLQVDGDLQLQSINFIGGQ-----PLRPQG-----PPMMPP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 TVLPSAQRFHIN--LCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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15-JUL-1998 (Rel. 36, Last annotation update)
GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFS-GNDIAFHFNPRFF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 PTYNPTLPYYQPIPGGLNVGMSVYIQG-VASEHMKRFFVNFVVGQDPGSDVAFHFNPRFD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 FHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 YVPPTGKSFAINFKVGSSGDIALHINPRMGNGTVVRNSLLNGSWGSEEKKITHN-PFGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPAPITQTVIHTVQSAPGQMFSTPAI - - PPMMYPHPAYPMPFITTILGGLYPSKSILLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 YPGP----GHCHQ----QLNSLPTMEGPPTFNP----PVPYFGRLQGGLTARRTIIIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 323;
                                                                        -!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 574; DB 1; Length 323
; Pred. No. 4.8e-39;
52; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E79EC0A9AB3990EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ductor.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00337; Gal-bind_lectin; 2. PROSITE; PS00339; Galabrin; 2. Galaptin; Lectin; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 GA
262 BE
35941 MW;
                                                                                                                                                                                                                                                                                                                                  EMBL; AB006781; BAA22165.1; -. EMBL; AF014838; AAC51763.1; -. HSSP; P17931; 1A3K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 35, Created)
(Rel. 35, Last sequ
(Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.9%;
38.2%;
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Best Local Similarity 38.29
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 3
256 2
323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEG4_PIG
Q29058; Q29296;
01-NOV-1997 (Rel
01-NOV-1997 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            library: analysis of 839 clones.";
Mamm. Genome 7:509-517(1996).
--- FUNCTION: GALECTIN THAT BINDS LACTOSE AND A RELATED RANGE OF
SUGARS. MAY BE INVOLVED IN THE ASSEMBLY OF ADHERENS JUNCTIONS.
--- SUBDMIT: MONOMER.
--- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 DIAFHFNPRFEDGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 ILFVQYFHRVPFHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 RRQKPPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAY--PMPFITTILGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PGPMP-NPG-----YPGPGKHNQQPCNLPCMEGAPTFNPPVPYKTRLQGG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 LYPSKSILLSGTVLPSAQRFHIN--LCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEER 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 SLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTH 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSSFN-PFAPGQYFDLSIRCGLDRFKVYANGQHLFDFSHRLSNFQGVDTLEIQGDVTLSY 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAF---SGSQAPYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFS-GN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95081129; PubMed-7989350;
Chiu M.L., Parry D.A.D., Feldman S.R., Klapper D.G., O'Keefe E.J.;
"An adherens junction protein is a member of the family of lactose-
                                                                                                                                                                            Winteroe A.K., Fredholm M., Davies W.; "Evaluation and characterization of a porcine small intestine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :: ||:| | : |:| : | :| DPFYEFGHRIPVQLVTHLQVDGDLTLQSINF----IGGQPAPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINKER.

GALATIN 2.

BETA-GALACTOSIDE (BY SIMILARITY).

BF -> GA (IN REF. 2).

H -> T (IN REF. 2).

728C761712B29343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.2%; Score 541; DB 1; Length 323; 36.5%; Pred. No. 2.1e-36; 1ve 54; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00337; Gal-bind_lectin; 2.
PROSITE; PS00309; GALAPTIN; FALSE_NEG.
Galaptin; Lectin; Repeat.
                                                                     J. Biol. Chem. 269:31770-31776(1994).
[2]
                                                                                                                                           TISSUE-Small intestine;
MEDLINE-96327607; PubMed-8672129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35852 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X79303; CAA55884.1; -. EMBL; F14653; CAA23179.1; -. HSSP; P17931; 1A3K.
                                                                                                                      SEQUENCE OF 1-140 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 AA;
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Best Local Simil
Matches 132; C
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 FSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVLPSAQRFHINLCSGNHIAFH 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 LNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWILCEAHCLKVAVDGQHLF 327
                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 FSTQT-----PYPNLAVPFFTSIPNGLYPSKSIVISGVVLSDAKRFQINLRCGGDIAFH
                                                                                                                                                                 ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION.
BETA-GALACTOSIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%; Score 535; DB 1; Length 14
70.3%; Pred. No. 2.5e-36;
ive 9; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN AAA65445).
BC95283D760DA515 CRC64;
                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
 144 AA
                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYYHRLRNLPTINRLEVGGDIQLTHVQT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00337; Gal-bind_lectin; 1.
PROSITE; PS00309; GALAPIN; 1.
Galaptin; Lectin; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 AA; 16065 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L36862; AAC42050.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L21711; AAA65445.1; -. HSSP; P17931; 1A3K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 104; Conservative
 STANDARD;
                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001079;
                                                               GALECTIN-5 (RL-18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                NCBI_TaxID=10116;
                        01-FEB-1996
01-FEB-1996
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MOD_RES
BINDING
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LEG5_RAT
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LEG6\_MOUSE

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188 NPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTV 247
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316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1928481;
                                                                                                                                                                                                             01-OCT-2000
                                                                                                                                                                                                                       01-OCT-2000
01-OCT-2000
                                                                                                                                                                                     LEG8_MOUSE
Q9JL15;
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                                                                                                                                                                        LEG8_MOUSE
                         160
                                                248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 273:2961-2970(1998).
-I- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 DGGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHRVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                          "Galectin-4 and galectin-6 are two closely related lectins expressed in mouse gastrointestinal tract."; J. Biol. Chem. 273:2954-2960(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 PYLSPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTG-FSGNDIAFHFNPRFE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWDKVVFNTKQSGRWGKEEEKS-MPFQKGKHFELVFMVMPEHYKVVVNGSPFYEYGHRLP
                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                        'Sequence, structure, and chromosomal mapping of the mouse Lgals6
                                                                                                                                                                                     Gitt M.A., Colnot C., Poirier F., Nani K.J., Barondes S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 301;
                                                                                                                                                                                                                                                                                              Gitt M.A., Xia Y.-R., Atchison R.E., Lusis A.J., Barondes
Leffler H.;
                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALAPTIN 2.
A -> V (IN AAC27244).
9A4DD09944EDFAB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.0%; Score 518; DB 1; 35.6%; Pred. No. 1.4e-34;
                      Created)
Last sequence update)
Last annotation update)
301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF026796; AAC04508.1; JOINED. AF026797; AAC04508.1: JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF026797; AAC04508.1; JOINED. AF026798; AAC04508.1; JOINED. AF026794; AAC27244.1;
PRT;
                                                                                                                                                                                                                                                                                                                                 encoding galectin-6.";
ol. Chem. 273:2961-2970(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00337; Gal-bind_lectin; 2. Galaptin; Lectin; Repeat.
                                                                                                                                                                       MEDLINE=98112847; PubMed=9446608;
                                                                                                                                                                                                                                                                                  MEDLINE=98112848; PubMed=9446609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF026799; AAC04508.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34112 MW;
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Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:107535; Lgals6.
InterPro; IPR001079; -.
 STANDARD;
          054891; 088352;
15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
01-OCT-2000 (Rel. 40,
                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 3
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                       STRAIN=129/SV
                                                           GALECTIN-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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                                                                        LGALS6
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                                                                                                           251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCINCHILTQEKWGWEEITYDMPFRKEKSFEIVFWVLKNKFQVAVNGRHVLLYAHRISP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 HRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPAN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 SPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFS---GNDIAFHFNPRFED 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbohydrate
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                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                          LPSAQRFHIN---LCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY).
11A20309AEF52C69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.4%; Score 467.5; DB 1; Length 316; 32.4%; Pred. No. 1.6e-30; ive 61; Mismatches 124; Indels 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL6/J; TISSUE=Kidney;
Maier C., Haeussler J., Roesch K., Moschgath E., Haeusler J.,
Vogel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression of
                                                                                                                                                                                              306 FSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHV 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The human Lgals-8 gene: genomic sequence and expre
prostate carcinoma tumour antigen (PCTA-1) and the
                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                      316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 BE
36161 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF218069; AAF27645.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00309; GALAPTIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galaptin; Lectin; Repeat.
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                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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BINDING
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                                                                                                                                                 DOMAIN
                                                                                                                                                              DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Su Z.-Z., Lin J., Shen R., Fisher P.E., Goldstein N.I., Fisher P.B.; "Surface-epitope masking and expression cloning identifies the human prostate carcinoma tumor antigen gene PCTA-1 a member of the galectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 PSAQRFHINLCSG--NHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSF 306
                                                                               208 TNARSFNVDLVAGKTRDIALHLNPRLNVKAFVRNSFLQDAWGEEERNI-TCFPFSSGMYF 266
                                 163 ALGLTQINRENIQK-PGKL-------OLSLPFEARLNASMGPGRTVVIKGEVN 207
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       189 PAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYPSKSILLSGTVL
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of a beta-galactoside-binding lectin related galectin-8 and identified in human lung carcinoma."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brichory F., Bidon N., Desrues B., Bourguet P., Le Pennec J.P.,
                                                                                                                                                                                                             LEGB_HUMAN STANDARD; PRT; 316 AA.
000214, 015215; Q9UP3; Q9UE26; Q9UP33; Q9UP32;
01-NOV-1997 (Rel. 35, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-1000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 90, LOSTATE CARCINOMA TUMOR ANTIGEN)
(POGG CARBOHYDRATE-BINDING PROTEIN) (POGG-CBP).
                                                                                                                                  EMITYCDVREFKVAINGVHSLEYKHRFKDLSSIDTLSVDGDIRLLDVRS 315
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                                                                                                                  307 SVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Hippocampus;
Hadari Y.R., Elsenstein M., Zakut R., Zick Y.;
"Galectin-8: on the road from structure to function.";
Trends Glycosci. Glycotechnol. 9:103-112(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:7252-7257(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L78132; AAB51605.1; -.
EMBL; X91790; CAA62904.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96293510; PubMed-8692978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lung carcinoma;
                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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LEG8_HUMAN
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EMBL; AF074001; AAD45403.1; -.
EMBL; AF074002; AAD45404.1; -.
EMBL; AF193805; AAF19370.1; ALT_INIT.
EMBL; AF193805; AAF19370.1; JOINED.
HSSP; P17931; IA3K.
INTERPROJ 17931; IA3K.
INTERPROJ 1797037; Gal-bind_lectin; 2.
Pfam; PF00337; Gal-bind_lectin; 2.
PROSITE; PS00309; GALAPTIN; 1.
Galaptin; Lectin; Repeat; Antigen; Alternative splicing; Polymorphism.
DOMAIN 1.153 GALAPTIN 1.
                                                                                                                                                                                                                                            BETA-GALACTOSIDE (BY SIMILARITY).
L -> LPSNRGGDISKIAPRTVYTKSKDSTVNHTLTCTKIP
                                                                                                                                                                                                                                                                             PMNYVSK (IN ISOFORM 2).
L -> LQTVSPSWDLQGHGSETFCSVLWTRVFLEIAFCRPI
GLTVASFQ (IN ISOFORM 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 TVLPSAQRFHINLCSG--NHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGYVVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHRVPF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 HRVDTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPAN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----DLQSTQASSLELTEISRENVPKSGTPQLSLPFAARLNTPMGPGRTVVVKG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPAVPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQTGFSGN---DIAFHFNPRFED 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 PAPITQTVIHTVQSAPGQMFSTPAIPPMMYPH---PAYPMPFITTILGGLYPSKSILLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 QSFSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                 /FTIG VAR_009710.
Y -> F (IN REF. 1 AND 2).
V -> M (IN REF. 2).
KRE -> QKEK (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1724C36085A0510A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 EKIDTLGIYGKVNIHSIGF----SFSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                            D -> A (IN REF. 2).
S -> V (IN REF. 1).
S -> R (IN REF. 2).
K -> Q (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.2%; Score 463.5; DB 1
31.8%; Pred. No. 3.3e-30;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-SUL-1998 (Rel. 36, Last annotation update)
GALECTIN-8 (30 KDA S-TYPE LECTIN) (RL-30).
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                                                                                                                                                                                                        LINKER.
GALAPTIN 2.
AF074000; AAD45402.1; -.
AF074001; AAD45403.1; -.
AF074002; AAD45404.1; -.
AF193806; AAF19370.1; ALT_INIT.
AF193805; AAF19370.1; JOINED.
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170
183
203
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316
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170
183
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316 AA;
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185
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SEQUENCE
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Q62665;
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Best Local
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Last sequence update)
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                     InterPro; IPR001079; -.
Pfam; PF00337; Gal-bind_lectin; 2.
PROSITE; PS00309; GALAPTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 39, Created)
(Rel. 39, Last sequ
(Rel. 39, Last anno
                                                                                        MM;
     EMBL; U09824; AAA66359.1; -
                                                                                        36038
                                                                                                               Query Match 23.7
Best Local Similarity 31.7
Matches 114; Conservative
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                                                                               248
316 AA;
                                               Galaptin; Lectin;
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30-MAY-2000
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044126;
                                                                                        SEQUENCE
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                                                       DOMAIN
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                                                                       DOMAIN
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LEG1_HAECO
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Pfam; PF00337; Gal-bind_lectin; 2. PROSITE; PS00309; GALAPTIN; 2.
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=6289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - DEVELOPMENTAL STAGE: VERY LOW LEVELS IN WHOLE EMBRYOS, HIGH LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||||||: :|||| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 
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Hadari Y.R., Paz K., Dekel R., Mestrovic T., Accili D., Zick Y.;
Hadari Y.R., Paz K., Dekel R., Mestrovic T., Accili D., Zick Y.;
"Galectin-8. A new rat lectin, related to galectin-4.";
J. Biol. Chem. 270:3447-3453(1995).
-i. FUNCTION: POSSESSES SUGAR BINDING AND HEMAGGLUTINATION ACTIVITY.
-i. SUBCELLULAR LOCATION: CYTOPLASMIC.
-i. TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, CARDIAC MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 RQKPPGVWPANPAPITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILGGLYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY
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31.7%; Pred. No. 1.8e-29;
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LINKER.
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STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN ADULT TISSUES.
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                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
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                                                                                                                                                                                                                                                                                                                      82;
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BETA-GALACTOSIDE (BY SIMILARITY).
84D319BF6F383750 CRC64;
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01-OCT-2000 (Rel. 40, Last annotation update)
32 KDA BETA-GALACTOSIDE-BINDING LECTIN (32 KDA GBP).
W09H1.6.
32 KDA BETA-GALACTOSIDE-BINDING LECTIN (GALECTIN 1)
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P36573;
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or send an email to license@isb-s1b.ch).
                                                                                    252 QRFHINLCSGN-HIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVWI 310
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                                                                                                                                                132 DTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPANPAP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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GALAPTIN 2.
BETA CALACTOSIDE (BY SIMILARITY).
5 5D191988B760B4AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BINDS GALACTOSE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
32 KDA BETA-GAACTOSIDE-BINDING LECTIN LEC-3 (32 KDA GBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.5%; Score 374; DB 1; Length 28 28.1%; Pred. No. 4.4e-23; ive 54; Mismatches 112; Indels
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                                                                                                                                                                                              311 LCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQ 354
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InterPro; IPR001079; -
Pfam; PF00337; Gal-bind_lectin; 2.
PROSTIP: PS00309; GALAPTIN; 1.
Galaptin; Lectin; Repeat; Multigene family.
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212 2
285 AA;
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97; Conserv
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Q09581;
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SEQUENCE
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                                                                             SECUENCE FROM N.A. MEDLINE-923483939; WEDLINE-92348399; BubMed-1639789; Hirabayashi J., Satoh M., Kasai K.-I.; Hirabayashi J., Satoh M., Kasai K.-I.; "Evidence that Caenorhabditis elegans 32-kDa beta-galactoside-binding protein is homologous to vertebrate beta-galactoside-binding lectins. CDNA cloning and deduced amino acid sequence."; J. Biol. Chem. 267:15485-15490(1992).
                                                                                                                                                                                                                        MEDIINE-97476274; PubMed-9334250;
Arata Y., Hirabayashi J., Kasai K.-I.;
"Structure of the 32-kDa galectin gene of the nematode Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVCNTRQNGSWGPEERKTHMPFQKGMPFDLCFLVQSSDFKVMVNGILFVQYFHRVPFHRV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 VPFSGTIQGGLQDGLQITVNGTVLSSSGTRFAVNFQT---GFSGNDIAFHFNPRFEDGGY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                     BETA-GALACTOSIDE (BY SIMILARITY).
ED9AE22AE37571DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6%; Score 414.5; DB 1; 29.4%; Pred. No. 2.4e-26; ive 54; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galaptin; Lectin; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALAPTIN 1.
GALAPTIN 2.
                                                                                                                                                                                                                                                                                          Biol. Chem. 272:26669-26677(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001079; -.
Pfam; PF00337; Gal-bind_lectin; 2.
PROSITE; PS00309; GALAPTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB000802; BAA22942.1; -... EMBL; AB000802; CAB04959.1; -... PIR; S27798; S27798. PIR; PX0062; PX0062. PIR; A42846. MO941.64; CE16576. HSSP; P17931; 1A3K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31809 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.4%
Matches 101; Conservative
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 202-220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 AA;
                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                               NCBI_TaxID=6239;
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10;

Gaps

Length 285;

99

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67 IVYNAYTKGTWGKEERAKN-PIKKGDDFDIRIRAHDSKFQVSINHKEVKNFEHRIPLNSV 125
                                                                                                                          192 ITQTVIHTVQSAPGQMFSTPAIPPMMYPHPAYPMPFITTILG-GLYPSKSILLSGTVLPS 250
                                                                                                                                                                                                   251 AQRFHINLCSGN-HIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQSFSVW 309
                                                                                                                                                                                                                     DTISVNGSVQLSYISFQNPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQKPPGVWPANPAP 191
                                                                                                                                                             -----YYPVPYESGIAADGLVPGKTLVVYGTPEKK 174
                                                                                                                                                                                                                                                                                          310 ILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLTHVQ 354
                                                                                       126 SHLSIDGDVVLNHVQ-----
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
GALECTIN-3 (GALATOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KDA LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; 244 AA PRT; STANDARD; P47953; 01-FEB-1996 LEG3\_CRILO CRILO 

Mehul B., Bawumia S., Martin S.R., Hughes R.C.; "Structure of baby hamster kidney carbohydrate-binding protein CBP30, an S-type animal lectin.";
J. Biol. Chem. 269:18258(1994).
-!- FUNCTION: GALACTOSE-SPECIFIC LECTIN WHICH BINDS IGE.
-!- SIMILARITY: THE C-TERMINAL DOMAIN BELONGS TO THE GALAPTIN
(S-LECTIN) FAMILY. TISSUE-Kidney; MEDLINE-94299546; PubMed-8027086; SEQUENCE FROM N.A. Cricetulus. NCBI\_TaxID=10030;

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InterPro; IPR001079; -.
Pfam; PF00337; Gal-bind\_lectin; 1.
PROSITE; PS00309; GALAPIN; 1.
Galaptin; Lectin; IgE-binding protein; Repeat; Phosphorylation; BY SIMILARITY EMBL; X78879; CAA55479.1; -HSSP; P17931; Acetylation. INIT\_MET MOD\_RES MOD\_RES 

ACETYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY CK1)
(BY SIMILARITY).
7 X 9 AA TANDEM REPEATS OF Y-P-G-X(3)-P[GS]-A. 98 42 51 60 69 REPEAT REPEAT DOMAIN REPEAT REPEAT

5 (APPROXIMATE).	6 (APPROXIMATE).	7 (APPROXIMATE).	GALAPTIN.	INTERCHAIN (BY SIMILARITY).	BETA-GALACTOSIDE (BY SIMILARITY).	MW; 8F99B9AA0BBA7D3F CRC64;	; Score 339; DB 1; Length 244;	9	NPRTVPVQPAFSTVP-FSQPVCFPPR-PRGRRQKPPGVWPANPAPI 192	PGQAPPGAYPGPTAPGAYPG	AYPHPAYPMPFITTILGGLYPSKSI	77 AYPGQPGASGAYPSAPGAYPAAGPYGAPTGALTVPYKLPLAGGVMPRMLITIMGTVK 133	PSAQREHINLCSGNHIAFHLNPRFDENAVVRNTQIDNSWGSEERSLPRKMPFVRGQS 305		FSVWILCEAHCLKVAVDGQHLFEYYHRLRNLPTINRLEVGGDIQLT 351	1   1   1   1   1   1   1   1   1   1
77	87	98	244	167	181	25608	17.78;	ď	AFSTVP-I	AGGY PG	SAPGOMES	SAPG1	HIAFHL	IIII VDIAFHF	/AVDGQHI	AVNDAHI
70	78	88	112	167	175	244 AA;		Milaricy 38.9 Conservative	PVQP	PGAWGNQPG	SOVTHIV	PGASGAYPS	FHINLCSGN	ILLNFLRGN	LCEAHCLKY	LVEADHFK
REPEAT	REPEAT	REPEAT	DOMAIN	DISULFID	BINDING	SEQUENCE	Query Match	best bocal similarity Matches 88; Conserv	149 NPRTV	17 NPQGW	193 TQT	77 AYPGQ	249 PSAOR	134 PNANR	306 FSVWI	192 FKIQV
FT	FT	FI	FT	FT	FT	Š	Ö	Wa	QΣ	ģα	ΟŻ	qq	Qy	Dp	Qγ	QQ

Search completed: August 1, 2001, 09:42:19 Job time: 684 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 1, 2001, 09:30:55 ; Search time 36.57 Seconds (without alignments) 29:975 Million cell updates/sec Run on:

US-09-485-951-1 178 1 NPRIVPVQPAFSIVPFSQPVCFPPRFRGRRQK 32 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues arched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	. p	0	O08573 mus musculu	Q9wvs8 mus musculu		epste	PO4672 glycine max		P35385 mus musculu	P53550 saccharomyc	_	P35442 homo sapien	_	Q9quk5 rattus norv	P19225 rattus norv	P41739 rattus norv	homo	рошо	mus m	snw	P04198 homo sapien	homo	уошо	selac		Q64700 mus musculu	O55081 rattus norv	rattus	P11799 gallus gall	homo sa	Q10116 neurospora	_	
SUMMARIES	OI OI	LEG9_HUMAN	LEG9_RAT	LEG9_MOUSE	MK07_MOUSE	CRK7_HUMAN	EBN2_EBV	NO44_SOYBN	ARNT_MOUSE	HSB7_MOUSE	PSU1_YEAST	MYCN_MARMO	TSP2_HUMAN	LI12_CAEEL	HSB7_RAT	CPCM_RAT	ARNT_RAT	RBL2_HUMAN	RON_HUMAN	GC1_MOUSE	GC1M_MOUSE	MYCN_HUMAN	IL2B_HUMAN	S145_HUMAN	HEM2_SELMA	CPCO_RAT	RBL2_MOUSE	RBL2_RAT	DSRA_RAT	KMLS_CHICK	HSB7_HUMAN	MATD_NEUCR	FTWH_MYCTU	
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æ	Query Match	100					30.3								28.4	28.4	28.4	28.1	28.1	27.8	27.8	27.8	27.8	27.8	27.5	27.5	27.5	27.5	27.5	27.5	27.2	27.2	27.2	0
	Score	178	104	94	62.5	52	54	53.5	52.5	51.5	51.5	51	21	51	50.5	50.5	50.5	20	20	49.5	49.5	49.5	49.5	49.5	49	49	49	49	49	49	48.5	48.5	48.5	
	Result No.		7	3	4	so.	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	,

010370 glycine max P09513 barley yell P04727 triticum ae P54704 dlctyostell 019012 erinaceus e P08328 escherichia P18089 homo sapien 015654 homo sapien 05649 mus musculu P54734 anabaena sp 094751 schizosacch 000423 glycine max
HMGB_SOYBN VPG_BYDVP GDA7_WHEAT PSPB_DIEDI A2AB_ERIEU A2AB_ERIEU A2AB_HUMAN TRI6_HUMAN TRI6_HUMAN TRI6_HUMAN TRI6_HUMAN HWA_ANGSP BUBI_SCHPO HMGA_SOYBN
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152 1153 313 379 391 409 476 559 564 1044
227.0 277.0 277.0 277.0 277.0 277.0 277.0
4 4 4 4 4 4 4 4 4 4 4 7 . 6 . 6 . 6 . 6 . 6 . 6 . 6 . 6 . 6 .

# ALIGNMENTS

RESULT 1 LEGG-HURAN  LEGG-LEGG-LEGG-LEGG-LEGG-LEGG-LEGG-LEG
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BINDING
BINDING
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J. Balol. Chem. 272:617-625(1997).

-I- FUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-
-I- FUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-
-I- FUNCTION: BINDS GALACTOSIDES RELEVANT TO THE BIOLOGY OF THE THYMOS (BY
SIMILARITY). MAY PROVIDE THE MOLECULAR BASIS FOR URATE FLUX ACROSS
CELL MEMBRANES, ALLOWING URATE THAY IS FORMED DURING PURINE
METABOLISM TO EFFLUX FROM CELLS AND SERVING AS AN ELECTROGENIC
TRANSPORTER THAT PLAYS AN IMPORTANT ROLE IN RENAL AND
GASTROINTESTINAL URATE EXCRETION. HIGHLY SELECTIVE TO THE ANION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSICAL SECRETORY PATHWAY (BY SIMILARITY).
-! FIRENATIVE PRODUCTS: AT LEAST 2 ISOFORMAS: A LONG FORM (SHOWN HERE) AND A SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: THE LONG FORM IS EXPRESSED EXCLUSIVELY IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegious (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CYTOPLASMIC. MAY ALSO BE SECRETED BY A NON-
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wada J., Kanwar Y.S.;
Identification and characterization of galectin-9, a novel beta-
galactoside-binding mammalian lectin.";
J. Biol. Chem. 272:6078-6086(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leal-Pinto E., Tao W., Rappaport J., Richardson M., Knorr B.A.,
                                                                                                                                                                                                                                                                ó
                                                                                                  DELA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
MISSING (IN SHORT ISOFORM).
G -> S (IN RFF ?)
                                                                                                                                                                                                                                        Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and functional reconstitution of a urate
                                                                                                                                                                                                                                                                                                                                                                               P97840; 008588; 035866; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 35, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotation update) GALECTIN-9 (36 KDA BETA-GALACTOSIDE BINDING LECTIN) (URATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LONG AND SHORT FORMS).
LEY; TISSUE-Kidney, and Small intestine;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                     K -> R (IN REF. 1).
S -> F (IN REF. 1).
P -> L (IN REF. 1).
E -> G (IN REF. 1).
4748C22FCAFA536A CRC64;
                                                                                                                                                                                                                                        Score 178; DB 1;
Pred. No. 4.8e-15;
                                                         Repeat; Alternative splicing.
                                                                                                                                            -> S (IN REF. 3)
-> R (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                       354 AA.
                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                 LINKER.
GALAPTIN 2.
                                                                                                                                                                                                                                                                                     1 NPRTVPVQPAFSTVPFSQPVCFPPRPRGRRQK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (SHORT FORM).
STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney;
MEDLINE-97150769; Pubmed-8995305;
                                  Pfam; PF00337; Gal-bind_lectin; 2. PROSITE; PS00309; GALAPTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97190351; PubMed=9038233;
                                                                                                                                                                                                                                       .100.0%;
100.0%;
                                                                                                                                                                                                     39518 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPORTER/CHANNEL) (UAT).
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Best Local Similarity 100.(
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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88
293
180
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                      InterPro; IPR001079;
HSSP; P17931; 1A3K.
                                                                                                                                                                                                   355 AA;
                                                           Galaptin; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116
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                                                                                                                              VARSPLIC
CONFLICT
CONFLICT
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                                                                                                                                                                                                   SEQUENCE
                                                                                                        BINDING
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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"Developmental regulation, expression, and apoptotic potential of galectin-9, a beta-galactoside binding lectin.";
J. Clin. Invest. 99:2452-2461(1997).
-!- FOUNCTION: BINDS GALACTOSIDES. MAY PLAY A ROLE IN THYMOCYTE-FPITHELIAL INTERACTIONS RELEAVAT TO THE BIOLOGY OF THE THYMUS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC. MAY ALSO BE SECRETED BY A NON-CLASSICAL SECRETORY PATHWAY.
-!- ALTERNATIVE PRODUCTS: AT LEAST. 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              galectin-9, a novel beta-
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BETA-GALACTOSIDE (BY SIMILARITY).
MISSING (IN SHORT ISOFORM).
6574F960B2ERF37C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galaptin; Lectin; Repeat; Alternative splicing; Ion transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.4%; Score 104; DB 1; Length 354; 59.4%; Pred. No. 5.8e-06;
                                                                      SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CD-1; TISSUE=Small intestine, and Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEG9_MOUSE STANDARD; PRT; 353 AA. 008573; 008572; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 NSTAAPVQPVFSTMQFSQPVQFPRMPKGRKQR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NPRTVPVQPAFSTVPFSQPVCFPPRPRGRROK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GALAPTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALAPTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wada J., Kanwar Y.S.,
Identification and characterization of
galactoside-binding mammalian lectin.";
J. Biol. Chem. 272:6078-6086(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001079; -.
Pfam; PF00337; Gal-bind_lectin; 2.
PROSITE; PS00309; GALAPIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97190351; PubMed-9038233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97298141; PubMed=9153289;
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354
GP
87
BE
292
BE
179
MI
39946 MW;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U59462; AAB51192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U72741; AAB68592.1; -. EMBL; U67958; AAB48591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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206
81
286
148
354 AA;
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PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY

us-09-485-951-1.rsp

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TISSUE SPECIFICITY: ACCENTUATED EXPRESSION IN LIVER AND THYMUS OF EMBRYO, DETECTED IN EMBRYONIC HEART, BRAIN, LUNG; LIVER, AND KIDNEY. HIGHLY EXPRESSED IN ADULT THYMUS, SMALL INTESTINE, AND LIVER, AND TO A LESSER EXTENT IN LUNG, KIDNEY, SPLEEN, CARDIAC, AND SKELETAL MUSCLE. BARELY DETECTABLE IN BRAIN AND RETICULOCYTE. THE LONG FORM IS EXPRESSED EXCLUSIVELY IN THE SMALL INTESTINE. DEVELOPMENTAL STAGE: THE EXPRESSION INCREASED WITH SUCCESSIVE STAGES OF EMBRYONIC DEVELOPMENT.
                                                                                                                                                                          DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALAPTIN 2.
BETA-GALACTOSIDE (BY SIMILARITY).
BETA-GALACTOSIDE (BY SIMILARITY).
MISSING (IN SHORT ISOPORM).
B54036F6E280C531 CRC64;
                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Galaptin; Lectin; Repeat; Alternative splicing.
DOMAIN 1 147 GALAPTIN 1.
DOMAIN 148 204 LINKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00337; Gal-bind_lectin; 2. PROSITE; PS00309; GALAPTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U55061; AAB51190.1; -.
EMBL; U55060; AAB51189.1; -.
HSSP; P17931; 1A3K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:109496; Lgals9.
InterPro; IPR001079; -
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148
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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0; Length 353; Indels Score 94; DB 1; Le: Pred. No. 9.8e-05; }; Mismatches 6; 52.8%; ilarity 66.7%; Conservative Similarity Query Match Best Local Simi Matches 18; g ò

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Gaps

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MEK5 AND ERK5 INTERACT SPECIFICALLY WITH ONE ANOTHER AND NOT WITH MEK1/ERK1 OR MEK2/ERK2 PATHWAYS (BY SIMILARITY).
-!- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE U1-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
MITOGEN-ACTIVATED PROTEIN KINASE 7 (EC 2.7.1.-) (EXTRACELLULAR SIGNAL-REGULATED KINASE 5) (ERK-5) (BMK1 KINASE). Kamakura S., Moriguchi T., Nishida E.; "Activation of the protein kinase ERK5/BMK1 by receptor tyrosine kinases: identification and characterization of a signaling pathway PHOSPHORYLATION (BY SIMILARITY).
DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN
TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 806 AA STANDARD; (Mouse). SEQUENCE FROM N.A. NCBI\_TaxID-10090; Mus musculus the nucleus. MK07\_MOUSE Q9WVS8; MK07\_MOUSE ESULT 

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ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (ACTIVATES THE KINASE) (BY SIMILARITY).
PHOSPHORYLATION (ACTIVATES THE KINASE) ROLE, IS ABSENT (BY SIMILARITY). SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE SUBFAMILY. ï Score 62.5; DB 1; Length 806; Pred. No. 1.6; Indels E7CC41C4BBDE0633 CRC64; PROTEIN KINASE. SIMILARITY 1; Mismatches PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1. PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1. PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1. PRO-RICH 1. PRO-RICH 2 POLY-ARG. (BY 4 TVPVQPAFSTV-PFSQPVCFPPRP 26 EMBL; AB019373; BAA82039.1; -. MW.; 35.1%; 62.5%; HSSP: P27703; 2ERK. MGD; MGI:1346347; Mapk7. InterPro; IPR000719; -. InterPro; IPR002290; -. PROSITE; PS01351; MAPK; 1. 87732 15; Conservative 347 465 524 700 69 84 182 219 806 AA; Query Match Best Local Similarity 434 521 578 61 84 182 221 Phosphorylation Transferase; SEQUENCE ACT\_SITE NP\_BIND BINDING MOD\_RES DOMAIN DOMAIN DOMAIN DOMAIN Matches a ŏ

CRK7\_HUMAN STANDARD; PRT; 1490 AA.
CRK7\_HUMAN STANDARD; PRT; 1490 AA.
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
CLCT-2000 (Rel. 40, Last annotation update)
RELATISION CYCLE 2-RELATED PROTEIN KINASE 7 (EC 2.7.1.-) (CDC2-CRK7 OR KIAA0904. Euteleostomi; Pines J.N., Kelly E.; Created protein kinase that colocalizes with interchromatin granule clusters."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. Craniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo SEQUENCE OF 266-1262 FROM N.A. Eukaryota, Metazoa, Chordata, Mammalia, Eutheria, Primates, Homo sapiens (Human). SEQUENCE FROM N.A. NCBI\_TaxID=9606; CRK7\_HUMAN 

MEDLINE-99156230; PubMed-10048485; Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,

TISSUE-Brain;

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     "DNA sequence and expression of the B95-8 Epstein-Barr virus genome."; Nature 310;207-211(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF LMP-1.
-!- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH THE NUCLEAR MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Virol. 65:2545-2554 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1;
Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                MEDLINE-90266473; PubMed-2161150;
Petti L., Sample C., Kieff E.;
Subnuclear localization and phosphorylation of Epstein-Barr virus latent infection nuclear proteins.";
Virology 176:563-574(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Activator; Nuclear protein; DNA-binding;
                                                                                                                                                                                                                                                                                                                    MEDLINE-91202599; PubMed-1850028;
Cohen J.I., Wang F., Kieff E.;
"Epstein Barr virus nuclear protein 2 mutations define essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Root nodules;
Sengupta-Gopalan C., Pitas J.W., Thompson D.V., Hoffman L.M.;
"Expression of host genes during root nodule development in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 1; Length 487; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-81146477; Pubmed-3822835;
Sandal N.N., Bojsen K., Marcker K.A.;
A small family of nodule specific genes from soybean.";
Nucleic Acids Res. 15:1507-1519(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       356 6 X 2 AA TANDEM REPEATS OF 52544 MW; DEF40D7F8ED61D1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                domains for transformation and transactivation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
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                                                                                           SUBCELLULAR LOCATION, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY - PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PRTVPVQPAFSTV -- PFSQPVCFPPRP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; V01555; CAA24877.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Gen. Genet. 203:410-420(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO44_SOYBN STANDARD; PRT P04672; P07127; 13-4NG-1987 (Rel. 05, Created) 13-4NG-1987 (Rel. 05, Last sequen 15-DEC.1998 (Rel. 37, Last annotau NODULIN 44 (N-44) (NODULIN E27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.3%;
Best Local Similarity 40.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -! - PIM: PHOSPHORYLATED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSFAC; T01618; -
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345
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        NA RANKA RAN
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RRRS -> SSSRSRHSSISPVRLPLNSSLGAELSRKKKERA
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE-84270667; PubWed=6087149;
Madr.NE-84270667; PubWed=6087149;
Badr R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Glbson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.;
                                                                                                          DNA Res. 5:355-364(1998).
-1- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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G -> D (IN REF. 2).
R -> K (IN REF. 2).
M -> T (IN REF. 2).
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P (BY SIMILARITY).
SIMILARITY.
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01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55;
Pred. No.
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ATP (BY S
BY SIMILA
POLY-ALA.
POLY-PRO.
POLY-PRO.
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NCBI_TaxID=10377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 PRTVPVQPAFSTVPFSQPVCFPP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF227198; AAF36401.1; -.
                                                                                     large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.9%;
52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB020711; BAA74927.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA; 164154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                      CDC2/CDKX SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000719; -. InterPro; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EBNA-2 NUCLEAR PROTEIN.
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745
1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P27703; 2ERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              639
745
1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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BINDING
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Matches

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CONFLICT
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HSB7_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. FORMS AN HETERODIMER WITH AHR, WITH HIFIA AS WELL AS WITH OTHER BHLH PROTEINS.
-I- SUBCELLULAR LOCATION: UBLOCATION:
-i- TISSUE SPECIFICITY: UBLOUTOUS.
-i- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THEN INITIATES TRANSCRIPTION OF A GENES INVOLVED IN THE ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translocator.";
J. Biol. Chem. 269:28038-28105(1994).
J. Biol. Chem. 269:28038-28105(1994).
J. FUNCTION: REQUIRED FOR ACTIVITY OF THE AH (DIOXIN) RECEPTOR. THIS PROTEIN IS REQUIRED FOR THE LIGAND-BINDING SUBGNIT TO TRANSLOCATE FROM THE CYTOSOL TO THE NUCLEUS AFTER LIGAND BINDING. THE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ARVL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR (ARNT PROTEIN) (DIOXIN RECEPTOR, NUCLEAR TRANSLOCATOR) (HYPOXIA-INDUCIBLE FACTOR 1 BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li H., Dong L., Whitlock J.P. Jr.; "Transcriptional activation function of the mouse Ah receptor nuclear
                                         -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION FACTORS.
  -!- INDUCTION: DURING NODULATION IN LEGUME ROOTS AFTER RHIZOBIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reisz-Porszasz S., Probst M.R., Fukunaga B.N., Hankinson O.; "Identification of functional domains of the aryl hydrocarbon receptor nuclear translocator protein (ARNT)."; Mol. Cell. Biol. 14:6075-6086(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                                                                                                                                                                                                                                                       DC4A6D3135EA46CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          791 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 53.5; D. Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 PPRPPUD--NIIPFPRPPNIVPFSPRGRRSK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG FORM).
STRAIN-C57BL/6; TISSUE-Liver;
MEDLINE-94344118; PubMed-8065341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6;
MEDLINE-95050586; Pubmed-7961746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I_MOUSE STANGE
PS7562; 060661;
PS7562; 060661;
01-0CT-1996 (Rel. 34, Created)
n 01-NOV-1997 (Rel. 35, Last seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                       360 AA; 39077 MW;
                                                                                                                                                                                                                                                                EMBL; X03979; CAA27618.1; -. EMBL; X05028; CAA28692.1; -. PIR; S09552; S09552.
                                                                                                                                                                                                                                                                                                                                                                                                                        30.1%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.8%,
".hoq 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF PAH PROCARCINOGENS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HIF-1 BETA).
                                                                                                                                                                                                                                                                                                                                Nodulation.
SEQUENCE
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ARNT_MOUSE
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                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSB7_MOUSE STANDARD, PRT; 169 AA.
HSB385, 090US2,
01-NOV-1995 (Rel.
HO. Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HEAT-SHOCK PROTEIN, BETA-7 (CARDIOVASCULAR HEAT SHOCK PROTEIN) (CVHSP)
(HEAT SHOCK PROTEIN 25 KDA 2) (PROTEIN P19/6.8).
HSPB7 OR HSP25-2 OR CVHSP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
PAS-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00785; NCTRNSLOCATR.
PROSSTEE, PS000384; HELIX_LOOP_HELIX; 1.
Nuclear protein; DNA-binding; Transcription regulation; Activator;
Alternative splicing; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cvHsp. A novel human small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
SDDEQSSADKERLARENHSEIERR -> TKFL (IN
SHORT ISOFORM).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae: Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52.5; DB 1; Length 791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization of cvHsp. A novel hums stress protein selectively expressed in cardiovascular and insulin-sensitive tissues "; J. Biol. Chem. 274:36592-36600(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S -> T (IN REF 2).
A -> R (IN REF 2).
T -> S (IN REF 2).
A -> C (IN REF 2).
A -> C (IN REF 2).
W; BDEB79E4BD75D452 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556 DPRFPEIYPSITADQSKGISSSTVPATQQLFSQGSSFPPNPR 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ARG.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20062883; PubMed-10593960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAS-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86977 MW;
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35.7%;
                                                                                                                                                                                                                    EMBL; U10325; AAA56717.1; -. EMBL; U14333; AAA61732.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.5
Best Local Similarity 35.7
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                   MGD; MGI:88071; Arnt.
InterPro; IPR000014; -.
InterPro; IPR001067; -.
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001092; -. InterPro; IPR003015; -. Pfam; PF00010; HLH; 1. Pfam; PF00989; PAS; 2.
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230
417
467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650
791 AA;
                                                                                                                                                                                                                                                                          HSSP; P22415; 1AN4
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MEDLINE=90370481; PubMed=2395655;
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                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00502; MUTTDOMAIN. PROSITE; PS00893; NUDIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  108667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYCN OR NMYC OR NMYC1.
Marmota monax (Woodchuck).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 30.4 Matches 14; Conservative
                                                                                                                                            S.POMBE SPAC19A8.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
  Dunckley T., Parker R.;
                                                                                                                                                                                                                                                                                                                          Pfam; PF00293; mutT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 970 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCN_MARMO
                                                                                                                                                                                                                                                                                                                                                                  Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                  Mouse News Lett. 84:76-77(1989).
-!- SUBUNIT: INTERACTS WITH C-TERMINAL DOMAIN OF ACTIN-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              de Antoni A., D Angelo M., Dal Pero F., Sartorello F., Pandolfo D., Pallavicini A., Lanfranchi G., Valle G.;
"The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces cerevisiae reveals an unusually high number of overlapping open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                        ·!- TISSUE SPECIFICITY: FOUND IN BOTH CARDIAC AND SLOW SKELETAL
                                                                                                                 -!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 169;
                                      Kluxen F.-W., Vandekerckhove J., Schoeffl F., Jockusch H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                      2 -> GD (IN REF. 2).
120F4ED8EA9D0E7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
MINAD DECAPPING PROTEIN 2 (PSUI PROTEIN)
DCP2 OR PSUI OR YNL118C OR N1917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   970 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        28.9%; Score 51.5; 33.3%; Pred. No. 7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 PVQPAFS-----TVPFSQPVCFPPRGR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 PMEKALSMFSDDFGSFMLPHSEPLAFPARPGGQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                             POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE~97245296; PubMed=9090055;
                                                                                                                                                                                                                                                                                                                                                                                        EΡ
                                                                                                                                                                                                                                                          EMBL; AJ243192; CAB63266.1; -. EMBL; AF155909; AAF20023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    18621 MW;
                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00299; ACRYSTALLIN. PROSITE; PS01031; HSP20; 1.
[2]
SEQUENCE OF 43-61 AND 76-87.
                                                                                                                                                                                                                                                                                  MGD; MGI:1352494; Hsp25-2.
InterPro; IPR001436; -.
InterPro; IPR002068; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.38
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (east 13:261-266(1997).
                                                                                                                                                                                                                                                                                                                          HSP20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERACTION WITH DCP1.
                                                                                                                                                                                                                                                                                                                                                              Heat shock; Chaperone
                                                                                                                                                                                                                                                                                                                                                                                                  .169 AA;
                                                                                                       (SOLEUS) MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-D273-10B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10508173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tzagoloff A.A.
                                                                                                                                                                                                                                                                                                                         Pfam; PF00011
                                                                                                                               FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSU1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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DR DR DR DR PFT SO SO
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SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fourel G., Tiollais P., Buendia M.-A.;
"Nucleotide sequence of the woodchuck N-myc gene (WN-mycl).";
Nucleic Acids Res. 18:4918-4918(1990).
-!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
                                                                                                                                                                       PERHAPS IN A PROCESS REQUIRING THE HYDROLYSIS OF A PYROPHOSPHATE BOND. DECAPPING IS A THE MAJOR PATHWAY OF MRNA DEGRADATION IN YEAST. IT OCCURS THROUGH DEADENYLATION, DECAPPING AND SUBSEQUENT
                                                                                                                          FUNCTION: REQUIRED FOR THE PRODUCTION OF ACTIVE DECAPPING ENZYME
"The DCP2 protein is required for mRNA decapping in Saccharomyces cerevisiae and contains a functional MutT motif."; EMBO J. 18:5411-5422(1999).
                                                                                                                                                                                                                                                                                                                                                                                                υΩ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                      5' TO 3' EXONUCLEOLYTIC DECAY OF THE TRANSCRIPT BODY. SUBUNIT: INTERACTS WITH DCP1. SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.9%; Score 51.5; DB 1; Length 970; 30.4%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
N-MYC PROJO-ONCOGENE PROTEIN (N-MYCI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MEDILINE-94010892; PubMed-8406456;
Labell T.L., Byers P.H.;
"Sequence and characterization of the complete human thrombospondin 2
cDNA: potential regulatory role for the 3' untranslated region.";
Genomics 17:225-229(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 12:421-429(1992).

-1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINGEN, FIBRONECTIN, LAMINN AND TYPE V. OCOLAGEN.
-1- SUBUNT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
-1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
-1- SIMILARITY: CONTAINS 1 VMFC DOMAINS.
-1- SIMILARITY: CONTAINS 3 TSP TYPE-1 DOMAINS.
-1- SIMILARITY: CONTAINS 7 TSP TYPE-1 DOMAINS.
-1- SIMILARITY: CONTAINS 7 TSP TYPE-3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92217961; PubMed-1559694; Labell T.L., MGGOOKEY Milewicz D.J., Disteche C.M., Byers P.H.; and Thrombospondin II: partial CDNA sequence, chromosome location, and expression of a second member of the thrombospondin gene family in
                                                                                      InterPro; ...

InterPro; ...

R Pfam; PF00010; HuH; 1.

R Pfam; PF01056; Myc_N_LEErm; 1.

R PRINTS; PR00044; LEUZIPPRMYC.

DR PROSITE; PS00038; HELIX_LOOP_HELIX; 1.

RW Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.

Nuclear protein; DNA-binding; Proto-oncogene; Phosphorylation.

ASP/GEU-RICH (ACIDIC).

ASP/GEU-RICH (ACIDIC).

HELIX-LOOP-HELIX MOTIF (BY SIMILARI' 17) 390

HELIX-LOOP-HELIX MOTIF (BY SIMILARI' 17) 390

HELIX-LOOP-HELIX MOTIF (BY SIMILARI' 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                          Score 51; DB 1; Length 460;
Pred. No. 24;
1; Mismatches 13; Indels
                                                                                                                                                                                                                                                               (BY SIMILARITY).
8A16686C82F5B02E CRC64;
                                                                                                                                                                                                                                       (BY SIMILARITY).
PHOSPHORYLATION (BY CK2)
                                                                                                                                                                                                                                                                                                                                                                          1 NPRIVPVQPAFS-----TVPFSQPVCFPPRGR 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
THROWNDSPONDIN 2 PRECURSOR.
THRSS OR TSP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1172 AA
                                                        EMBL; X53673; CAA37712.1; -. EMBL; X53674; CAA37712.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 560-1172 FROM N.A.
                                                                                                                                                                                                                                                                          460 AA; 49192 MW;
                                                                                                                                                                                                                                                                                                              28.78;
38.58;
                                                                                                                                                                                                                                                                                                              Query Match 28.7
Best Local Similarity 38.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                 InterPro; IPR001092; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fibroblast;
                                                                                                                                                                                                                                                  259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TSP2_HUMAN P35442;
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              humans."
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                                                                                                                                                                                                                        InterPro; IPR000561; -.
InterPro; IPR001084; -.
InterPro; IPR0010084; -.
InterPro; IPR0010007; -.
Pfam; PF001009; EGF; 2.
Pfam; PF00090; tsp_1; 3.
Pfam; PF00090; tsp_1; 3.
PROSITE; PS00122; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01208; TSP1; 3.
PROSITE; PS01208; WPC; 1.
Glycoprotein; Cell adhesion; Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CALCIUM-BINDING (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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INTERCHAIN (PROBABLE).
INTERCHAIN (PROBABLE).
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60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           THROMBOSPONDIN 2. HEPARIN-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2AC7BB230E44C6F5 CRC64;
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CHORD (GLCNAC.
N'LINKED (GLCNAC.
N'LINKED (GLCNAC.
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TSP TYPE-13.
TSP TYPE-13.
EGF-LIKE 1.
EGF-LIKE 2.
CAI
EGF-LIKE 3.
TSP TYPE-31.
TSP TYPE-3 2.
TSP TYPE-3 3.
TSP TYPE-3 3.
TSP TYPE-3 4.
TSP TYPE-3 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TERMINAL.
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N-LINKED
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                                                                                                                                    PIR: A42173; A42173. HSSP; P00740; IIXA. MIN, 188061; -.
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588
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710 71
1069 106
1172 AA;
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Best Local Similarity
Matches 13; Conserv
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STANDARD;

LI12\_CAEEL P14585;

RESULT 13 LI12\_CAEEL Caenorhabditis elegans.

SEQUENCE FROM N.A.

[2] SEQUENCE FROM N.A.

HID DATE OF THE SERVICE OF THE SERVI

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EGF-LIKE 1.
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 9.
EGF-LIKE 9.
EGF-LIKE 10.
EGF-LIKE 11.
EGF-LIKE 12.
LIN/NOTCH 1.
LIN/NOTCH 2.
          PROSITE; PS00010. ASX_HYDROXYL; 3.
PROSITE; PS00102; EGF_1; 12.
PROSITE; PS01186; EGF_2; 11.
PROSITE; PS01187; EGF_CA; 2.
Differentiation; Repeat; ANK repeat; EGF-like domain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                      LIN-12 PROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                             CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
MEDLINE=88334747; PubMed=3419531;
Yochem J., Weston K., Greenwald I.;
"The Caenorhabditis elegans lin-12 gene encodes a transmembrane protein with overall similarity to Drosophila Notch.";
Nature 335:547-550(1988).
                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-07-2000 (Rel. 40, Last annotation update)
LIN-12 PROTEIN PRECURSOR.
LIN-12 OR R107.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch)
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EMBL; M12069; AAA70191.1; -.
EMBL; 214092; CAA78474.1; -.
PIR; S06434. S06434. HSSP; P00740; IIXA.
WORMPEP; R107.8; CE00274.

InterPro; IPR000561; -. InterPro; IPR000800; -.

Pfam; PF00008; EGF; 13. Pfam; PF00023; ank; 4. InterPro; IPR001881; -.
InterPro; IPR002110; -.

notch;

PF00066;

Pfam;

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                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 274:36592-36600(1999).
-1- SUBUNIT: INTERACTS WITH C-TERMINAL DOMAIN OF ACTIN-BINDING PROTEIN 280 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
:TA-7 (CARDIOVASCULAR HEAT SHOCK PROTEIN) (CVHSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krief S., Faivre J.-F., Robert P., Le Douarin B., Brument-Larignon N., Lefrere I., Bouzyk M.M., Anderson K.M., Greller L.D., Tobin F.L., Souchet M., Bril A.; "Identification and characterization of cvHsp. A novel human small stress protein selectively expressed in cardiovascular and insulin-sensitive tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                       Gaps
                               (POTENTIAL)
    (POTENTIAL)
                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- TISSUE SPECIFICITY: FOUND IN BOTH CARDIAC AND SKELETAL MUSCI-1- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
                   (POTENTIAL)
                                                                                                                                                       4;
                                                                                                                         Length 1429;
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N-LINKED (GLCNAC. .) (POTEN
MM; 255EDD7A62C025DB CRC64;
                                                                                                                                                       Indels
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                                                                                                                         51; DB 1;
No. 72;
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Pred. No. 5.7;
                                                                                                                                                       Mismatches
                                                                                                                       Score Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Heart;
MEDLINE-20062883; PubMed-10593960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF155910; AAF20024.1; -.
TE; PS01031; HSP20; PARTIAL.
                                                                                                                                                                                                                196 STVEFKQPVCFLEISADHPDGR 217
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                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last seq
01-0CT-2000 (Rel. 40, Last anno
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33.3%;
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54.58;
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1429 AA;
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Best Local Similarity
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Q9QUK5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     rat hepatocytes.";
Proc. Natl. Acad. Sci. U.S.A. 87:9746-9750(1990).
-!- FUNCTION: CYTOCHROMES P450 ARE A GROUD OF HEME-THIOLATE
MONOOXYGENAES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
ACIDS, AND XENOBLOTICS.
-!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
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                                                                                                                                                      Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                               01-NOV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 2C22 (EC 1.14.14.1) (CYPIIC22) (P450 MD) (P450 P49).
CYP2C22 OR CYP2C-22 OR P450MD.
                                                                                                                                                                                                                                                                                                                                                                                                                      Emi Y., Chijiiwa C., Omura T.;
"A different cytochrome P450 form is induced in primary cultures of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001128; -
InterPro; IPR002401; -
Pfam; PF00067; p450; 1,
PRINTS; PR00463; EP450.
PRINTS; PR00468; CYTOCHROME_P450; 1,
PROSITE; PS00086; CYTOCHROME_P450; 1,
Microsome; Endoplasmic reticulum.
                                                                                                                                                                                                                                                          MEDLINE=90370497; PubMed=2395662; Nagata K., Sasamura H., Miyata M., Shimada M., Yamazoe Y., Kato R. "cDNA and deduced amino acid sequences of a male dominant P-450Md
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OXIDIZED FLAVOPROTEIN + H(2)0.
-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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Pred. No. 29;
2; Mismatches 10; Indels
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V -> L (IN REF. 2).
T -> I (IN REF. 2).
P -> L (IN REF. 2).
E -> O (IN REF. 2).
E -> O (IN REF. 2).
                  489 AA.
                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 18:4934-4934(1990)
                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                PRT;
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                                                 01-NOV-1990 (Rel. 16, Created)
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Best Local Similarity 44.4
Matches 12; Conservative
                  STANDARD;
                                                                                                                                         Rattus norvegicus (Rat).
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PIR; A39257; A39257.
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Gaps

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Indels

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6; Mismatches

11; Conservative

Matches

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Qy Db

Search completed: August 1, 2001, 09:42:18 Job time: 683 sec

us-09-485-951-1.rst

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1 MRCOt4405 Sorghum b
1 H3005B03-3 NIA Mous
2 HS_5478_B2_B02_T7A
1 HVSMEC0016L07f Hord
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Email: capabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lmage/image.html
Seq primer: MI3 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotan Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 439)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AW403229 439 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BK0-abb-a-03-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone
AZ922294 N
BG063271 N
AQ883620 N
BG310261 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3055397"
/clone=lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B_(LT1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 CCAGCCTGTCTGTTTCCCACCCAGGCCCAGGGGGCCCAGACAAAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 32
Gaps: 0
Percent Identity: 100.000
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       181
393
559
849
126.09
295.75
435.70
689.85
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                                                                                                                                                                                                                                                                                                                                             IMAGE: 3055397 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cocation/Qualifiers
139.04
132.39
129.37
125.79
                                                                                                                                                                                                                                                                                                                                                                             AW403229.1 GI:6922108
   64.00
64.00
64.00
64.00
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .439
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US-09-485-951-1 x AW403229
                                                                                                                                                                      seq_name: gb_est46:AW403229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est53:AW886539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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   gb_gss34:AZ922294
gb_est96:BG063271
gb_gss18:AQ883620
gb_est99:BG310261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV432219 AV432219 Porphyra yezc
AV435766 AV435766 Porphyra yezc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV436271 Porphyra yez
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BP250023A20F6 Soares
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                                                                                                                                                                                                                                                               -MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgn2_1/Uspf0_spool/Us0948551/runat_31072001_202942_13211/app_query.fasta_1.504
-Q-/cgn2_1/Uspf0_spool/Us09485551/runat_31072001_202942_13211/app_query.fasta_1.504
-DEST_-QFMT-fastap -SUFFIX=rst -GAPOP=12.000 -GAPOEXT=4.000
-GAPOEXT=0.0FO -LOOPEL-0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-GGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -PECAPOP=6.000
-GGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOPE-6.000
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTPHT-pfs -NORM-ext -MINLEN-0
-ALIGN=15 -MODE-LOCAL -OUTPHT-PREADS=1
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BF242509 601876084F1 NIH_MC
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AV432219
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                                                                                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Wed Aug

AW886539.1 GI:8048551

DEFINITION ACCESSION

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uman.

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.iigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Mi3 Reverse
Class: BAC ends.
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QV3-BT0537-221299-048-c06 BT0537 Homo sapiens cDNA, mRNA sequence.
AW373817
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 97 c 145 g 63 t
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 394)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Slmon, M. and
                                 AQ279515 394 bp DNA GSS 22-NOV-1998
CITBI-E1-251LL11.TR CITBI-E1 HOMO Sapiens genomic clone 251LL11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1998)
Other GSSs: CITBI-E1-2511L11.TF
Other GSSs: CITBI-E1-2511L11.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
711: 301 838 0200
Fax: 301 838 0208
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US-09-485-951-1 x AQ279515/rev
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                                                                                                               DNA sequence.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC1-OT0083-220 300-021-22&t4=1)
Seq primer: puc 18 forward 19 56 primer: puc 18 forward 19 57 primer: puc 18 fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: ovary; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue many and cona amplification were performed under low
                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 780)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
AW886539 780 bp mRNA EST 23-MAY-2000
RCI-OT0083-220300-021-c02 OT0083 Homo sapiens CDNA, mRNA sequence.
AW886539
                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Hara Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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FEATURES

rel: +55-11-2704922

Simpson, A.J.

TITLE

JOURNAL MEDLINE COMMENT

from: 1 to: 780

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Tel: +55-11-2704922
Fax: +55-11-2707001
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32 a 208 c 176 g 148 t l others
                                                                                                                                                                                                                                      Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-BT0537-
2212999-048-c06&t3=1999-12-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 664.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 535)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unlymblished (2001)
Contact: Genoscope
                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AL559554 535 bp mRNA EST 16-FEB-2001
DEFINITION AL559254 LTI_NFL008_TC2 Homo sapiens cDNA clone CSODJ012YD19 5
prime, mRNA sequence.
ACCESSION AL559254
VERSION AL559254.1 GI:12904575
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AsnProArgThrValProValGlnProAlaPheSerThrValProPheSe 17
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5.467 Gaps: 0
93.750 Percent Identity: 93.750
                    1 (bases 1 to 665)
HGGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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                                                                                                                                                                                                                   rel: +55-11-2704922
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US-09-485-951-1 x AW373817
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TITLE
JOURNAL
COMMENT
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AUTHORS
                                                            TITLE
JOURNAL
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was primed with a NotI-oligo(df) primer. Five prime end
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cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filangelifetech.com URL:
http://fulllength.invitrogen.com"

13 a 183 c 126 g 89 t 40 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QV3-ET0203-081200-525-a04 ET0203 Homo sapiens cDNA, mRNA sequence.
BF883419
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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20202663
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                                                                                              Location/Qualifiers
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Mammalia; Eutheria;
1 (bases 1 to 404)
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5.429
87.500
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US-09-485-951-1 x AL559254
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US-09-485-951-1 x BF143767
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BF181157
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TITLE
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KEYWORDS
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                                                                                                                                                                        1. .404
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/dev_stage="Adult"
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30 a 150 c 87 g 87 t
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Email: Gapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequen
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-ET0203-081200-525-a04&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 404.
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Gaps: 0
Percent Identity: 90.909
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plate: LLAM9274 row: k column: 13
High quality sequence stop: 685.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 5.364
Percent Similarity: 100.000
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BF143767
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COMMENT
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AUTHORS
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a 210 c 161 g 171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS BF181157 909 bp mRNA EST 31-OCT-2000
DEFINITION 601805820F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4036661 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases 1 to 90% NIH-WGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAM9312 row: h column: 06
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Gaps: 0
Percent Identity: 74.074
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/lab_host="DH10B"
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High quality sequence stop: 678.
Location/Qualifiers
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/clone="IMAGE:4036661"
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Percent Similarity: 85.185
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NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF533977 1165 bp mRNA EST 11-DEC-2000 602075139F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4212273 5',
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="FFW""
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone_1ib="NCI_CGAP_Li9"
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Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs.remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.m column: 10
High quality sequence stop: 735.
                                                                                                                                                                                                                                                                                                                                                                  1 others
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Percent Identity: 74.074
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/organism="Mus musculus"
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US-09-485-951-1 x BF181157
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BF533977
                                                         "HIN
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LOCUS BF533977
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Quality:
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Far: 217 333 5998

Fax: 217 244 5617

Email: h-levinéuluc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

to H. A. Lewin and J. E. Womack. Base Calling/Quallty Scores: PHRED

from Washington University Genome Center. Vector Trimmi g:

Cross_match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Lewin, H. A. W. M. M. M. M. M. W. M. Keck Center for Comparative and Functional Genomics W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: placenta; Vector: p1713Pac; Site_1: EcoRI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. " 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF046316 323 bp mRNA EST 10-OCT-2000 BP250002B10C9 Soares normalized bovine placenta Bos taurus cDNA clone BP250002B10C9 5', mRNA sequence.
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/clone="BP250002B10C9"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
                                                                                                                                                                                                                                                                   491 CCTGTCCAGCCTGTCTTCTCCACAGTGCAGTTCTCTCAGCCAGTCCAGTT 540
                                                                                                                                                                                                                              6 ProValGlnProAlaPheSerThrValProPheSerGlnProValCysPh 22
Percent Identity: 74.074
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Insert Length: 323 Std Error: 0.00
Plate: BP250002B10 row: C column: 9
Seq primer: AGCGGATAACAATTTCACACAGGA
                                                                                                                                                                from: 1 to: 1165
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Location/Qualifiers
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FORWARD: TAATACGACTCACTATAGGG
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                                                                                                                                                             to: BF533977
                                                                alignment_block:
US-09-485-951-1 x BF533977
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us-09-485-951-1.rst

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 590)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AA521753 590 bp mRNA EST 17-JUL-1997
DEFINITION v115h07.r1 Barstead mouse proximal colon MPLRB6 Mus musculus CDNA
clone IMAGE:903901 5' similar to SW:LEG4_RAT P38552 GALECTIN-4 ;'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:524565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:903901"
/clone_lib="Barstead mouse proximal colon MPLRB6"
/de_stage="7 day juvenile"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                 1 AsnProArgThrValProValGlnProAlaPheSerThrValProPheSe 17
                                                                         Length: 27
Gaps: 0
Percent Identity: 62.963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
Conteact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
                                                                                                                                                            Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 401. Location/Qualifiers
                                                                                                                                      17 rGlnProValCysPheProProArgProArgGlyArgArg 30
      to: 539
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      to: AW655379 from: 1
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US-09-485-951-1 x AA521753
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                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
AA521753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 539)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUL-2000
                                                                                                                                                                                                                                          79 AACATCCGCGCAGCTCCCAAGCAGCCCGCCTGCTCCAAGGTGCAGTTCTC 128
                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
Locus AM655379 539 bp mRNA
FFINITION 106111 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
FESSION AW655379
                                                                                                                                                                                                  1 AsnProArgThrValProValGlnProAlaPheSerThrValProPheSe 17
Gaps: 0
Gaps: 0
Percent Identity: 66.667
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Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TP1: 402 762 4396
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTCCCAGTCACGACG
Plate: 87 row: D column: 12.
Seq primer: ATTTAGGTGACATARG.
Location/Qualifiers
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW655379.1 GI:7421205
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4.333
80.000
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      104.00
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E 1 (bases 1 to 327)

E (cono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Itawa, M., Kadota, K., Rawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kogawa, J., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Salto, H., Sata, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shizaki, T., Sogabe, Y., Suzuki, H., Taqwa, A., Shizaki, F., Tominaga, N., Toya, Y., Vano, K., Yasunishi, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yokota, Y., Watanaba, J., Toya K., Yoshihide Hayashizaki, Y., Genome Exploration Research Genome Exploration Research Genome Exploration Research Genome Exploration Research Genome Exploration Genome Exploration Research Research
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URL:http://genome-resertc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp/
Carninci,P., Nushiyama,Y., Westover,A., Itch,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itch,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB144606 327 bp mRNA EST 28-JUN-2000 BB144606 RIKEN full-length enriched, adult female vagina Mus musculus cDNA clone 9930026003 3' similar to U81829 Mus musculus calumenin mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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                                                                                                               6 ProvalGlnProAlaPheSerThrValProPheSerGlnProValCysPh 22
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
   to: 590
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/clone="9930026D03"
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to: AA521753
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COMMENT
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TITLE

FEATURES

REFERENCE AUTHORS

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/dev_stage="adult"
//lab_host="slite" | Site_2: BamHI: cDNA library was fala_hote="slite_1: SalI: Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was GAGAGAAGAACCAAGAGCTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I bases 1 to 94.0cl nih, gov/. I har WGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs.rdmail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Caboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Plate: LLCM917 row: n column: 01
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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BF127246
BF127246.1 GI:10966286
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/clone_lib="NiH_WGC_76"
/lab_nost="DH10B (T1 phage-resistant)"
/note="Organ: liver. Vector: PDNR-LIB (Clontech); Site_l:
Sfil (ggccgoctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGCGGGCGCATG-4T(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
Plate: LLCM1335 row: m column: 18
High quality sequence stop: 191.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
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Percent Identity: 38.298
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/clone_lib="NIH_MGC_75"
/clone="IMAGE:4071744"
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BG402468.1 GI:13295916
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3-09-485-951-1 x BF127246
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LOCUS BG402468
                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
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849 CCAAAAACAATACCAATACAACCCACACGCAAGAAACGGCACCCACGAA 898
                                                                                                                                                                                                                                                               2 ProArgThrValProValGlnProAla...PheSerThrValProPheSe 17
                                                                                                                                                                               Gaps: 1
Percent Identity: 48.148
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                                                                                                                                                                                                                                                                                                                  899 GGAGCCAAACGCCGCACCGCCGCCCCAGA 929
                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: BG402468 from: 1
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3.205
81.481
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US-09-485-951-1 x BG402468
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